

# Analysis of Interconnection Evolution by rpoB Gene in Multidrug Resistant of Mycobacterium tuberculosis in Iranian Isolates

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**Background:** This is the first genetic biodiversity study of *M. tuberculosis* in Iran. Thus, we investigated the genetic patterns of strains isolated in the first survey of anti-tuberculosis drug-resistance by *rpoB* gene as part of the Global Project of Anti-tuberculosis Drug Resistance Surveillance (IPI, Iran).

**Material and Method:** A 411-bp fragment of the *rpoB* gene, containing the sequence of the 81-bp *rpoB* fragment, was amplified by PCR and the *rpoB* gene fragments of tuberculosis strains were sequenced using the Amersham auto sequencer. For analysing tree evolution used method UPGMA and Neighbour-Joining. Clinical isolates (34/163) were analysed by using sequencing gene *rpoB* and genotyped by program MEGA.

**Results:** The results were compared with the international database. MDR was 14% in never treated patients and 8% in previously treated patients. Mutations in *rpoB* gene and *katG* genes were detected in 95% and 84% of the MDR strains, respectively. Two clusters were found to be identical by the four different analysis methods, presumably representing cases of recent transmission of MDR tuberculosis. The other strains are divided into 2 groups: group A - similar to the standard and Eastern strains (China, Taiwan) and group B - strains of another genotype. They are grouped separately on the dendrogram and became prevalent in Iran (they are called Iranian residential strains).

**Conclusion:** This study gives a first overview of the *M. tuberculosis* strains circulating in Iran during the first survey of anti-tuberculosis drug-resistance. It may aid in the creation of a national database that will be a valuable support for further studies.

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# Distribution of Pulmonary Tuberculosis and TB Drug Resistance in a Hospital Setting in Papua New Guinea

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Tuberculosis (TB) is increasing at alarming rates in Papua New Guinea (PNG). WHO revealed a staggering incidence rate of 104/100 000 population in 2004, which coincided with a mere 20% case-detection rate. TB drug resistance has never been investigated, however is anticipated to be present in high proportions. This hospital-based perspective study was aimed at investigating the distribution of pulmonary TB and TB drug resistance, with specific objectives of establishing drug resistance profile for this study setting and providing a form of guideline for future drug resistance monitoring and therapy approaches in hospital settings in PNG. Patients were recruited on routine presentation at Modilon Hospital, Madang Province. Direct smear microscopy was carried out followed by sputum processing using 4% sodium hydroxide (NaOH). Culture and drug resistance testing were performed using the BACTEC MGIT960 Culture System. A total of 339 new TB patients were recruited between January and December of 2006 and 53% were positive for acid-fast bacilli. Two hundred and forty samples were cultured and 30.4% (73/240) showed positive growth. Drug resistance testing was successfully carried out in 69 isolates, of which 92.8% were from new TB cases. Overall drug resistance was therefore, observed in 17.4% (11 new cases and 1 previously treated case). Multiple drug resistant TB (MDR-TB) was detected in 8.7% (5 new TB cases and 1 previously treated case). Resistance to at least streptomycin was the most common (75% of all drug resistant cases) followed by resistance to at least rifampicin (50%). This study provided the first evidence of TB drug resistance in PNG. MDR-TB alone was the most common form of TB drug resistance observed in this study. Madang province is rated as median risk for TB, thus further investigation is required in high risk areas of TB in PNG.

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# The 60 Years Battle Against Tuberculosis in Hong Kong - A Review of the Past and a Projection Into the 21st Century

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**Background:** In October 2008, the Hong Kong Tuberculosis, Chest and Heart Diseases Association will be celebrating